

OM nucleic - nucleic search, using SW model  
Run on: April 15, 2005, 22:23:59 ; Search time 525 Seconds  
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```

RESULT 1
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent NO. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Schung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin
; TITLE OF INVENTION: Strains and Isolation Process of (HMG)-COA Reductase
; FILE REFERENCE: 004135_P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494

```





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OM nucleic - nucleic search, using sw model  
 Run on: April 15, 2006, 22:09:44 ; Search time 7424 Seconds  
 (without alignments)  
 11324.281 Million cell updates/sec

Title: US-09-991-518C-4  
 Perfect score: 1479  
 Sequence: 1 agagttcgatccgttcag.....agtcgtacaaaggtagccgt 1479

Scoring table: IDNITY-NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
 Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

Genbank:  
 1: gb\_bti:  
 2: gb\_ini:  
 3: gb\_env:  
 4: gb\_omn:  
 5: gb\_over:  
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 7: gb\_pnti:  
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 9: gb\_rrn:  
 10: gb\_sts:  
 11: gb\_xy:  
 12: gb\_uni:  
 13: gb\_vrl:  
 14: gb\_mtg:  
 15: gb\_pbl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

#### ALIGNMENTS

19	1459	98.6	1480	1	AY562200	AY562200 Salinospo	
20	1454	98.3	1479	1	AY562203	AY562203 Salinospo	
21	1429	96.6	1429	1	AY878316	AY878316 Salinospo	
c	22	1414.2	95.6	38146	1	AY524043	AY524043 Micromono
C	23	1409.4	95.3	1479	1	AY040255	AY040255 Micromono
24	1405.8	95.1	1507	1	AB193564	AB193564 Micromono	
25	1405.8	95.1	1508	1	AB193563	AB193563 Micromono	
26	1404.8	95.0	1508	1	AB193562	AB193562 Micromono	
27	1403.6	94.9	1482	1	AB159779	AB159779 Micromono	
28	1403	94.9	1470	1	MRRN16S	X92596 M. melanospo	
29	1402.4	94.8	1476	1	MGL16SRRN	X92615 M. globoosa 1	
30	1401.8	94.8	1476	1	MCI16SRRN	X92617 M. citrea 16	
31	1401.4	94.8	1479	1	AY040624	AY040624 Micromono	
32	1400.8	94.7	1471	1	MEP16SRRN	X92608 M. echinoplo	
33	1400.2	94.7	1474	1	MEA16SRRN	X92618 M. echinopur	
34	1400.2	94.7	1476	1	MRRN16S	X92595 M. purpurea	
35	1399.8	94.6	1480	1	AY534220	AY534220 Actinomyces	
36	1399.4	94.6	1477	1	MEN50635	AJ750635 Micromono	
37	1399	94.6	1466	1	MERN16S	X92597 M. echinoplo	
38	1399	94.6	1466	1	MRI16SRRN	X92612 M. rhodorang	
39	1398.6	94.6	1477	1	MAU245712	AJ745712 Micromono	
40	1398.6	94.6	1477	1	MRO16SRRN	X92631 M. rosaria 1	
41	1396.6	94.4	1509	1	AU783889	AJ783889 Micromono	
42	1396.6	94.4	1509	1	AU783992	AJ783992 Micromono	
43	1396.5	94.4	1510	1	AU783994	AJ783994 Micromono	
44	1396	94.4	1472	1	MEB16SRRN	X92655 M. echinobru	
45	1395.4	94.3	1476	1	MN16RRNA	X92602 M. narsashino	

Database :

Genbank:  
 1: gb\_bti:  
 2: gb\_ini:  
 3: gb\_env:  
 4: gb\_omn:  
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 6: gb\_pnt:  
 7: gb\_pnti:  
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 9: gb\_rrn:  
 10: gb\_sts:  
 11: gb\_xy:  
 12: gb\_uni:  
 13: gb\_vrl:  
 14: gb\_mtg:  
 15: gb\_pbl:

#### ALIGNMENTS

RESULT 1	AY040619	AY040619	1479	bpg	DNA	linear	BCT	08-JUN-2005
LOCUS								
DEFINITION								
Salinopora sp. CNH643 16S ribosomal RNA gene, partial sequence.								
ACCESSION	AY040619	2	GI:67043491					
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
Bacteria; Actinobacteria; Actinomycetida; Actinomycetales;								
Micromonosporaceae; Micromonosporales;								
I (bases 1 to 1479)								
REFERENCE								
AUTHORS								
Mincer, T.J., Jensen, P.R., Kauffman, C.A. and Fenical, W.								
TITLE								
Widespread and persistent populations of a major new marine								
actinomycete taxon in ocean sediments								
Appl. Environ. Microbiol. 68 (10), 5005-5011 (2002)								
JOURNAL								
PUBLISHED								
REFERENCE								
AUTHORS								
Mincer, T.J., Jensen, P.R., Kauffman, C.A. and Fenical, W.H.								
TITLE								
Direct Submission								
JOURNAL								
Submitted (15-JUN-2001) Marine Chemistry, Scripps Institution of								
Oceanography, UCSD, 8602 La Jolla Shores Dr., La Jolla, CA								
9203-2004, USA								
REFERENCE								
Jensen, P.R., Mincer, T.J. and Fenical, W.								
AUTHORS								
TITLE								
Direct Submission								
Submitted (10-JUN-2005) CMEB, Scripps Institution of Oceanography,								
Mail Code 0204, La Jolla, CA 92093, USA								
Sequence update by submitter								
COMMENT								
On Jun 8, 2005 this sequence version replaced gi:22474396.								
FEATURES								
Location/Qualifiers								
source								
1. -1479								
organism="Salinopora arenicola"								
/mol_type="genomic DNA"								
/strain="CMEB43"								
/db_xref="Taxon:168697"								
rrna								
ORIGIN								
/product="16S ribosomal RNA"								
Query Match								
100.0%								
Score 1479;								
DB 1;								
Length 1479;								

Sun Apr 16 12:42:18 2006

us-09-991-5

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OM nucleic - nucleic search, using sw model

Run on: April 16, 2006, 00:04:50 ; Search time 788 Seconds  
(without alignments)  
7559.850 Million cell updates/sec

Title: US-09-991-518C-4  
Perfect score: 1479  
Sequence: 1 agagttgatccctggcttag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
1: /SIDSS5/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

2: /SIDSS5/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

3: /SIDSS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

4: /SIDSS5/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

5: /SIDSS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

6: /SIDSS5/ptodata/2/pubpna/US03\_NEW\_PUB.seq1:\*

7: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

8: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq1:\*

9: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*

10: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq3:\*

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12: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*

13: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*

14: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*

15: /SIDSS5/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:35:29 ; Search time 524 Seconds  
 (without alignments)  
 8702.075 Million cell updates/sec

Title: US-09-991-518C-4  
 Perfect score: 1479  
 Sequence: 1 agagtttgcctggcttag.....agtcgttaacaaggtagccgt 1479

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6753657 seqs, 1541544009 residues

Total number of hits satisfying chosen parameters: 13507314

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

1: /SIDSS/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*

2: /SIDSS/ptodata/2/pna/US06\_NEW\_COMB.seq:\*

3: /SIDSS/ptodata/2/pna/US07\_NEW\_COMB.seq:\*

4: /SIDSS/ptodata/2/pna/US08\_NEW\_COMB.seq:\*

5: /SIDSS/ptodata/2/pna/US09\_NEW\_COMB.seq:\*

6: /SIDSS/ptodata/2/pna/US10\_NEW\_COMB.seq:\*

7: /SIDSS/ptodata/2/pna/US10\_NEW\_COMB.seq1:\*

8: /SIDSS/ptodata/2/pna/US11\_NEW\_COMB.seq:\*

9: /SIDSS/ptodata/2/pna/US11\_NEW\_COMB.seq1:\*

10: /SIDSS/ptodata/2/pna/US11\_NEW\_COMB.seq2:\*

11: /SIDSS/ptodata/2/pna/US11\_NEW\_COMB.seq3:\*

12: /SIDSS/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
c	1183.6	80.0	1487	8	US-11-335-686-1	Sequence 1, Appli
	1177.2	79.6	1443	7	US-10-521-336-1	Sequence 1, Appli
	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
	868.2	58.7	1555	5	US-09-941-095-160	Sequence 160, App
	865.4	58.5	1554	11	US-11-348-413-10825	Sequence 10825, A
	863.6	58.4	1504	10	US-11-273-617-10	Sequence 10, Appli
	858	58.0	1587	10	US-11-273-617-8	Sequence 8, Appli
	851.8	57.6	1538	11	US-11-348-413-12	Sequence 12, Appli
	851.8	57.6	1541	8	US-11-370-472-18	Sequence 18, Appli
	850.2	57.5	1513	8	US-11-370-472-10	Sequence 10, Appli
	845.8	57.2	1540	8	US-11-370-472-30	Sequence 30, Appli
	845.4	57.2	1541	8	US-11-370-472-19	Sequence 19, Appli
	843.8	57.1	1550	8	US-11-370-472-64	Sequence 64, Appli
	843.8	57.1	1550	8	US-11-370-472-65	Sequence 65, Appli
	843.8	57.1	1550	8	US-11-370-472-66	Sequence 66, Appli
	843.8	57.1	1550	8	US-11-370-472-67	Sequence 67, Appli
	843.8	57.1	1550	8	US-11-370-472-68	Sequence 68, Appli
	843.8	57.1	1550	8	US-11-370-472-69	Sequence 69, Appli
	843.8	57.1	2160266	7	US-10-513-024-1373	Sequence 1373, Ap
	843.2	57.0	1568	10	US-11-273-617-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:19:09 ; Search time 8961 Seconds  
 (without alignment)  
 9125.795 Million cell updates/sec

Title: US-09-991-518C-4

Perfect score: 1479

Sequence: I aggtttatccggctcag.....agtcgtacaacaaggtagcgt 1479

Scoring table: IDENTITY\_NTC

Gapext 1.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents\_NA\_Main:\*

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3: /cgn2_6/ptodata/1/pna/PCTRUSC_COMB_seq:*
4: /cgn2_6/ptodata/1/pna/US056_COMB_seq:*
5: /cgn2_6/ptodata/1/pna/US075_COMB_seq:*
6: /cgn2_6/ptodata/1/pna/US076_COMB_seq:*
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16: /cgn2_6/ptodata/1/pna/US086_COMB_seq:*
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18: /cgn2_6/ptodata/1/pna/US088_COMB_seq:*
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Sun Apr 16 12:42:18 2006

us-09-9

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 23:49:41 ; Search time 1329 Seconds  
(without alignments)  
9202.716 Million cell updates/sec

Title: US-09-991-518C-4  
Perfect score: 1479  
Sequence: 1 agagtttgatcctggctcag.....agtcgttaacaaggtagccgt 1479

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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